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RAW SEQUENCE LISTING

DATE: 11/06/2002

PATENT APPLICATION: US/10/004,115A

TIME: 14:53:55

Input Set : A:\73727249.app

Output Set: N:\CRF4\11062002\J004115A.raw

3 <110> APPLICANT: ASAKO, HIROYUKI
 4 MATSUMURA, KENJI
 5 SHIMIZU, MASATOSHI
 6 ITO, NOBUYA
 7 WAKITA, RYUHEI
 9 <120> TITLE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE
 10 4-HALO-3-HYDROXYBUTANOATE
 12 <130> FILE REFERENCE: 7372-72249
 14 <140> CURRENT APPLICATION NUMBER: 10/004,115A
 C--> 15 <141> CURRENT FILING DATE: 2002-10-23
 17 <150> PRIOR APPLICATION NUMBER: JP 2000-372704
 18 <151> PRIOR FILING DATE: 2000-12-07
 20 <150> PRIOR APPLICATION NUMBER: JP 2001-006144
 21 <151> PRIOR FILING DATE: 2001-01-15
 23 <150> PRIOR APPLICATION NUMBER: JP 2001-026594
 24 <151> PRIOR FILING DATE: 2001-02-02
 26 <150> PRIOR APPLICATION NUMBER: JP 2001-175175
 27 <151> PRIOR FILING DATE: 2001-06-11
 29 <160> NUMBER OF SEQ ID NOS: 37
 31 <170> SOFTWARE: PatentIn Ver. 2.1
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 325
 35 <212> TYPE: PRT
 36 <213> ORGANISM: Penicillium citrinum
 38 <400> SEQUENCE: 1
 39 Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro
 40 1 5 10 15
 42 Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
 43 20 25 30
 45 Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
 46 35 40 45
 48 Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
 49 50 55 60
 51 Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
 52 65 70 75 80
 54 Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
 55 85 90 95
 57 Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
 58 100 105 110
 60 Phe Leu Val His Trp Pro Ile Ala Glu Lys Asn Gly Gln Gly Glu
 61 115 120 125
 63 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 64 130 135 140

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66 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
67 145                               150                               155                               160
69 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
70                               165                               170                               175
72 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
73                               180                               185                               190
75 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
76                               195                               200                               205
78 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
79 210                               215                               220
81 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
82 225                               230                               235                               240
84 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
85                               245                               250                               255
87 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
88                               260                               265                               270
90 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
91 275                               280                               285
93 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
94 290                               295                               300
96 Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
97 305                               310                               315                               320
99 Lys Asn Leu Ser Ala
100                               325
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 978
105 <212> TYPE: DNA
106 <213> ORGANISM: Penicillium citrinum
108 <220> FEATURE:
109 <221> NAME/KEY: CDS
110 <222> LOCATION: (1)..(975)
112 <400> SEQUENCE: 2
113 atg tct aac gga aag act ttc aca ttg agc aac ggc gtc aag att cct 48
114 Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro
115 1 5 10 15
117 ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc 96
118 Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
119 20 25 30
121 tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac 144
122 Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
123 35 40 45
125 tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt 192
126 Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
127 50 55 60
129 gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc 240
130 Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
131 65 70 75 80
133 tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg 288
134 Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp

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135		85		90		95	
137	tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg	336					
138	Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met						
139		100		105		110	
141	ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag	384					
142	Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu						
143		115		120		125	
145	ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432					
146	Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr						
147		130		135		140	
149	gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat	480					
150	Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp						
151	145		150		155	160	
153	cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt	528					
154	Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu						
155		165		170		175	
157	gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc	576					
158	Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile						
159		180		185		190	
161	gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc	624					
162	Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe						
163		195		200		205	
165	tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac	672					
166	Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn						
167		210		215		220	
169	cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac	720					
170	Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn						
171	225		230		235	240	
173	gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc	768					
174	Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala						
175		245		250		255	
177	tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc	816					
178	Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro						
179		260		265		270	
181	aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac	864					
182	Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp						
183		275		280		285	
185	ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc	912					
186	Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val						
187		290		295		300	
189	aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc	960					
190	Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala						
191	305		310		315	320	
193	aag aac ctg tct gcg tga	978					
194	Lys Asn Leu Ser Ala						
195		325					
198	<210> SEQ ID NO: 3						
199	<211> LENGTH: 17						
200	<212> TYPE: PRT						

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Input Set : A:\73727249.app

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201 <213> ORGANISM: Penicillium citrinum
203 <400> SEQUENCE: 3
204 Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn Gln Val
205   1                               5               10               15
207 Pro
210 <210> SEQ ID NO: 4
211 <211> LENGTH: 10
212 <212> TYPE: PRT
213 <213> ORGANISM: Penicillium citrinum
215 <400> SEQUENCE: 4
216 Ile Pro Gly Val Phe Gly Thr Phe Ala Ser
217   1                               5               10
220 <210> SEQ ID NO: 5
222 <400> SEQUENCE: 5
W--> 223 000
226 <210> SEQ ID NO: 6
227 <211> LENGTH: 14
228 <212> TYPE: PRT
229 <213> ORGANISM: Penicillium citrinum
231 <220> FEATURE:
232 <221> NAME/KEY: MOD_RES
233 <222> LOCATION: (6)..(7)
234 <223> OTHER INFORMATION: Variable amino acid
236 <400> SEQUENCE: 6
W--> 237 Tyr Glu Asp Val Leu Xaa Xaa Ile Asp Asp Ser Leu Lys Arg
238   1                               5               10
241 <210> SEQ ID NO: 7
243 <400> SEQUENCE: 7
W--> 244 000
247 <210> SEQ ID NO: 8
248 <211> LENGTH: 20
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
255 <400> SEQUENCE: 8
256 ggaacytgrt tytggswacc                                     20
259 <210> SEQ ID NO: 9
260 <211> LENGTH: 20
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
267 <220> FEATURE:
268 <221> NAME/KEY: modified_base
269 <222> LOCATION: (3)
270 <223> OTHER INFORMATION: a, c, t, g, other or unknown
272 <220> FEATURE:
273 <221> NAME/KEY: modified_base

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Input Set : A:\73727249.app

Output Set: N:\CRF4\11062002\J004115A.raw

274 <222> LOCATION: (6)
 275 <223> OTHER INFORMATION: a, c, t, g, other or unknown
 277 <220> FEATURE:
 278 <221> NAME/KEY: modified_base
 279 <222> LOCATION: (9)
 280 <223> OTHER INFORMATION: a, c, t, g, other or unknown
 282 <400> SEQUENCE: 9

W--> 283 tangcnacng gcataatatt

20

286 <210> SEQ ID NO: 10
 287 <211> LENGTH: 20
 288 <212> TYPE: DNA
 289 <213> ORGANISM: Artificial Sequence
 291 <220> FEATURE:
 292 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 294 <220> FEATURE:
 295 <221> NAME/KEY: modified_base
 296 <222> LOCATION: (3)
 297 <223> OTHER INFORMATION: a, c, t, g, other or unknown
 299 <220> FEATURE:
 300 <221> NAME/KEY: modified_base
 301 <222> LOCATION: (6)
 302 <223> OTHER INFORMATION: a, c, t, g, other or unknown
 304 <220> FEATURE:
 305 <221> NAME/KEY: modified_base
 306 <222> LOCATION: (9)
 307 <223> OTHER INFORMATION: a, c, t, g, other or unknown
 309 <400> SEQUENCE: 10

W--> 310 tangcnacng gcataatggt

20

313 <210> SEQ ID NO: 11
 314 <211> LENGTH: 20
 315 <212> TYPE: DNA
 316 <213> ORGANISM: Artificial Sequence
 318 <220> FEATURE:
 319 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 321 <220> FEATURE:
 322 <221> NAME/KEY: modified_base
 323 <222> LOCATION: (3)
 324 <223> OTHER INFORMATION: a, c, t, g, other or unknown
 326 <220> FEATURE:
 327 <221> NAME/KEY: modified_base
 328 <222> LOCATION: (6)
 329 <223> OTHER INFORMATION: a, c, t, g, other or unknown
 331 <220> FEATURE:
 332 <221> NAME/KEY: modified_base
 333 <222> LOCATION: (9)
 334 <223> OTHER INFORMATION: a, c, t, g, other or unknown
 336 <400> SEQUENCE: 11

W--> 337 tangcnacng gcatgatatt

20

340 <210> SEQ ID NO: 12

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/004,115A

DATE: 11/06/2002
TIME: 14:53:56

Input Set : A:\73727249.app
Output Set: N:\CRF4\11062002\J004115A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 6,7
Seq#:9; N Pos. 3,6,9
Seq#:10; N Pos. 3,6,9
Seq#:11; N Pos. 3,6,9
Seq#:12; N Pos. 3,6,9
Seq#:13; N Pos. 3,6,9
Seq#:14; N Pos. 3,6,9
Seq#:15; N Pos. 14,63,116,148,185,235,346,460,463,485,489,491,520,524,593
Seq#:15; N Pos. 602,682
Seq#:18; N Pos. 14
Seq#:19; N Pos. 434,440,443,448,458,467,475,506,510,517,522,533,535,583,584
Seq#:19; N Pos. 607,616,634,639,648,651,652,659,662,664,670,671,690,693,695
Seq#:19; N Pos. 702,717,723,728,734

VERIFICATION SUMMARY

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Input Set : A:\73727249.app

Output Set: N:\CRF4\11062002\J004115A.raw

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:223 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:
L:237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:244 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:60
L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:120
L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:180
L:517 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:300
L:519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:420
L:520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:480
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:540
L:522 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:600
L:523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:660
L:561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:420
L:743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:480
L:744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:540
L:745 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:600
L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:660
L:747 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:720
L:1038 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (31) SEQUENCE: